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O|  |O  IntelliGenetics
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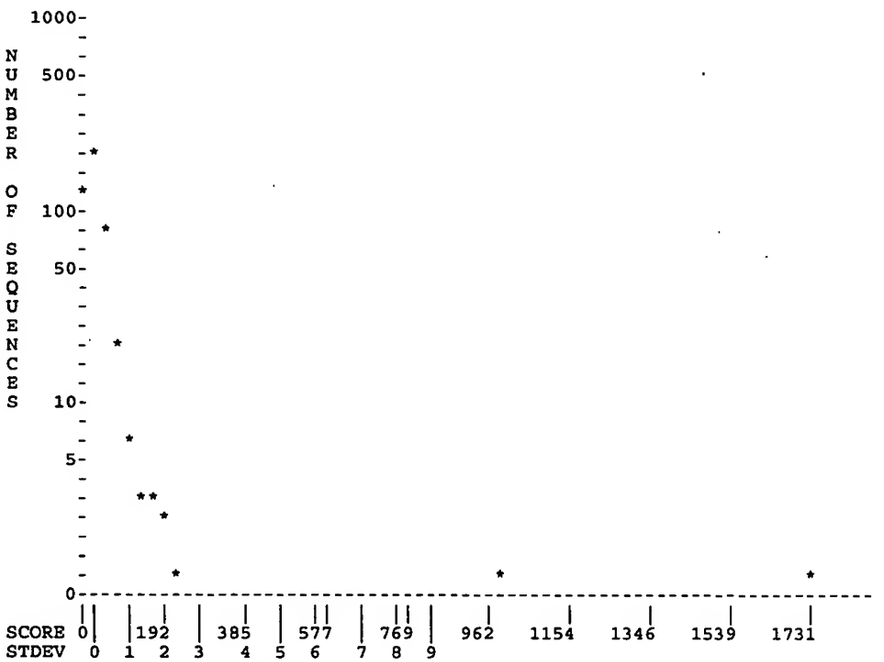
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-006-130a-129.res made by tport on Fri 20 Feb 104 15:36:33-PST.


Query sequence being compared:US-10-006-130A-129 (1-2213)
Number of sequences searched:                409
Number of scores above cutoff:               409

      Results of the initial comparison of US-10-006-130A-129 (1-2213) with:
        File : 6525174.seq
        File : US09374046A.seq
```

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                              PARAMETERS

Similarity matrix       Unitary     K-tuple                      4
Mismatch penalty              1     Joining penalty             30
Gap penalty                5.00     Window size                500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                          SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                             48           42          89.04

Times:                      CPU                    Total Elapsed
                       00:00:01.07                 00:00:02.00

Number of residues:                498643
Number of sequences searched:         409

Number of scores above cutoff:        409

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                                    Init. Opt.
Sequence Name     Description                          Length Score Score  Sig. Frame
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                    **** 18 standard deviations above mean ****
  1. US-09-374-046A-3 Sequence 3, Application U   3508  1731  2150  18.90   0
                    **** 10 standard deviations above mean ****
  2. US-09-205-258-20 Sequence 200, Application   1707   998  1638  10.67   0


1. US-10-006-130A-129 (1-2213)
   US-09-374-046A-3 Sequence 3, Application US/09374046A

Initial Score     =   1731  Optimized Score  =   2150  Significance = 18.90
Residue Identity =     95%  Matches          =   2204  Mismatches   =     9
Gaps              =     106  Conservative Substitutions              =     0

    X       10        20        30        40        50        60        70
    GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTGCTCATCGTTT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTGCTCATCGTTT
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    GCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTTATCTGAAAAGGTTAGTCAGCTGATGG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTTATCTGAAAAGGTTAGTCAGCTGATGG
          80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    AATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACAAGTTCCGTCGCCTTGTGAAAGCCCCACCGA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACAAGTTCCGTCGCCTTGTGAAAGCCCCACCGA
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    GAAATTACTCCGTTATCGTCATGTTCACTGCTCTCCAACTGCATAGACAGTGTGTCGTTTGCAAGCAAGCTG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GAAATTACTCCGTTATCGTCATGTTCACTGCTCTCCAACTGCATAGACAGTGTGTCGTTTGCAAGCAAGCTG
     220       230       240       250       260       270       280

   290       300       310       320       330       340       350       360
    ATGAAGAATTCCAGATCCTGGCAAACTCCTGGCGATACTCCAGTGCATTCACCAACAGGATATTTTTTGCCA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATGAAGAATTCCAGATCCTGGCAAACTCCTGGCGATACTCCAGTGCATTCACCAACAGGATATTTTTTGCCA
   290       300       310       320       330       340       350       360

          370       380       390       400       410       420       430
    TGGTGGATTTTGATGAAGGCTCTGATGTATTTCAGATGCTAAACATGAATTCAGCTCCAACTTTCATCAACT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGGTGGATTTTGATGAAGGCTCTGATGTATTTCAGATGCTAAACATGAATTCAGCTCCAACTTTCATCAACT
          370       380       390       400       410       420       430

        440       450       460       470       480       490       500
    TTCCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGCTGAGCAGA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TTCCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGCTGAGCAGA
        440       450       460       470       480       490       500

       510       520       530       540       550       560       570
    TTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCCCAAATTATGCTGGTCCCC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCCCAAATTATGCTGGTCCCC
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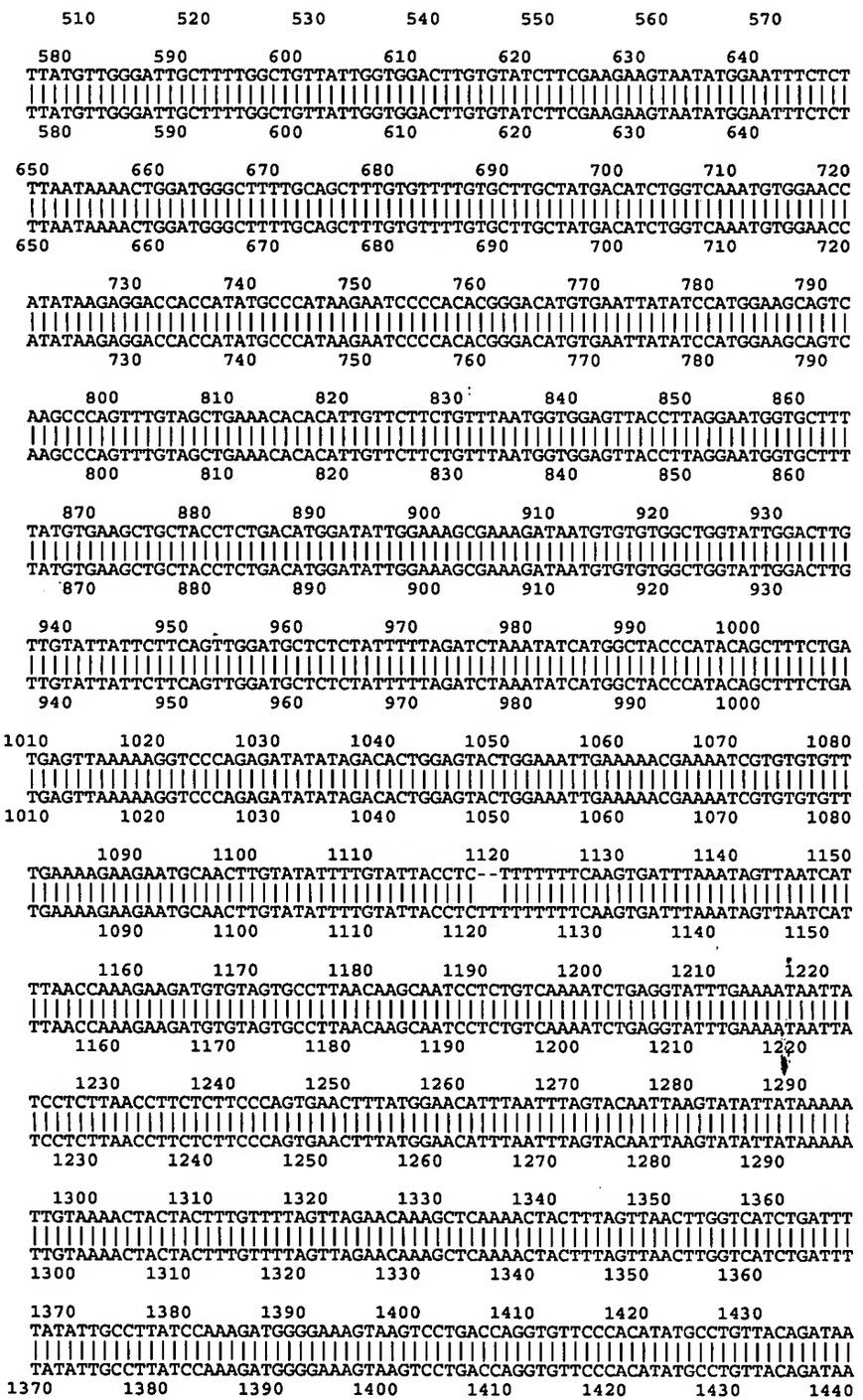

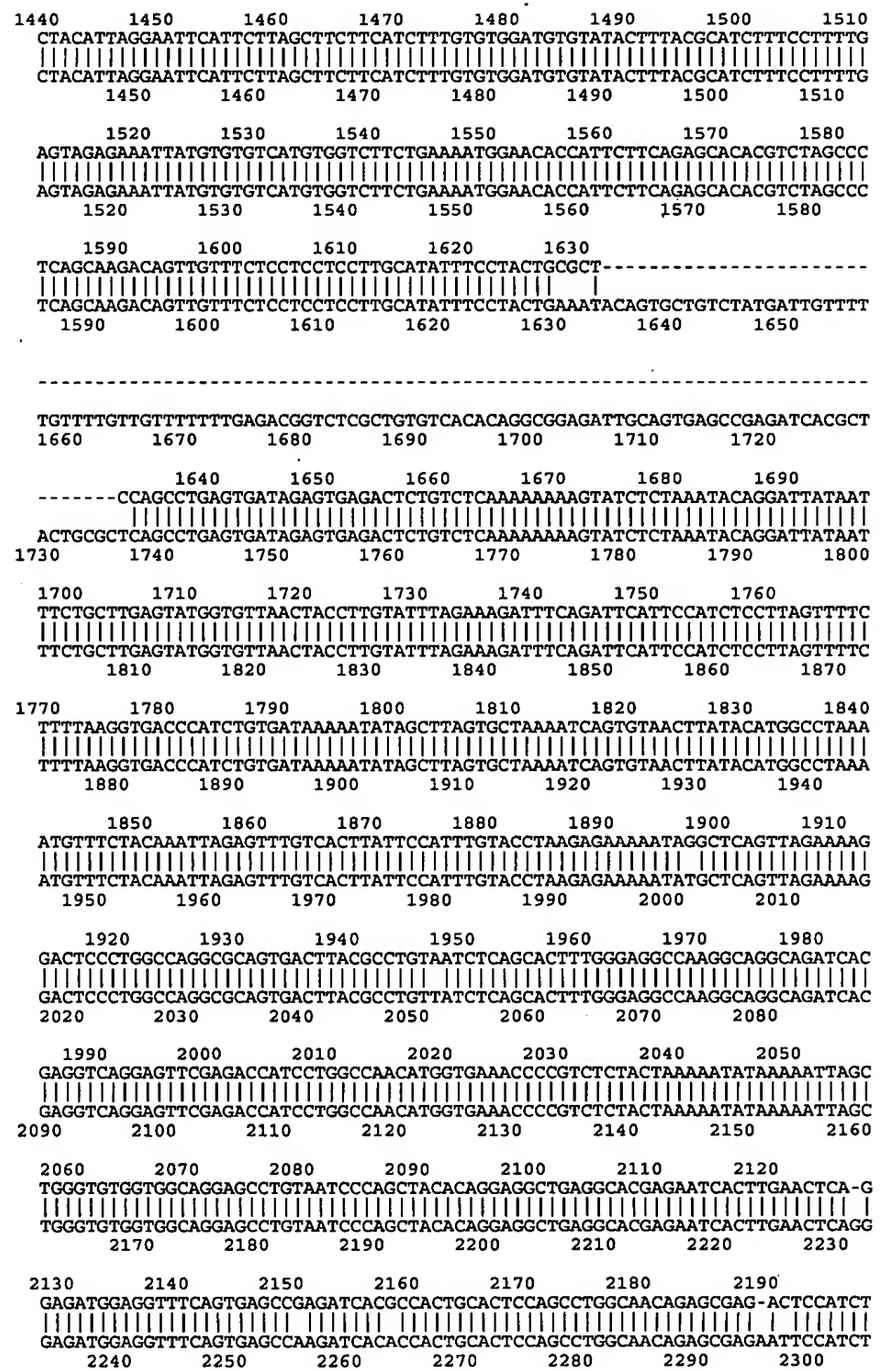

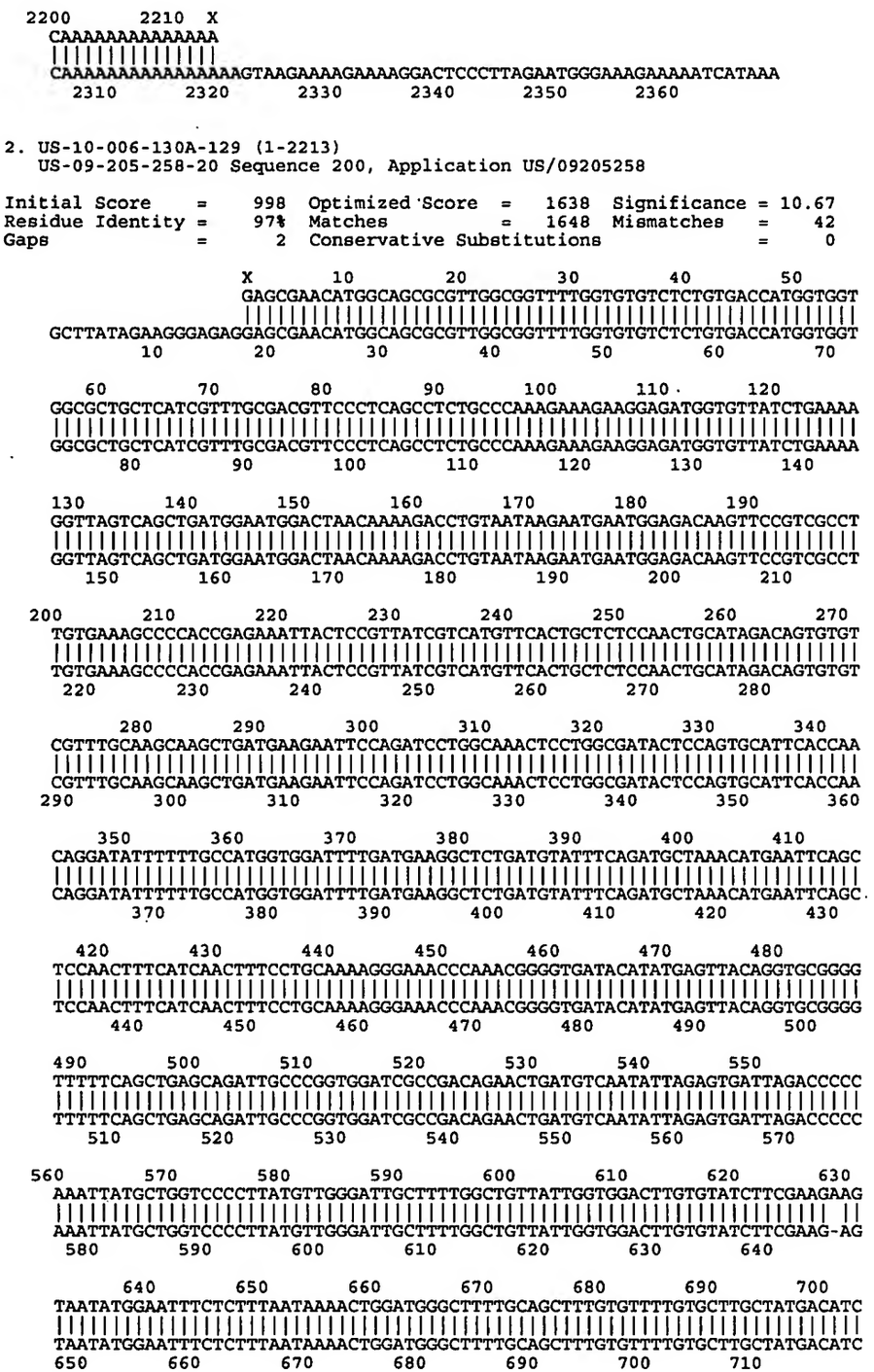

2. US-10-006-130A-129 (1-2213)
US-09-205-258-20 Sequence 200, Application US/09205258

Initial Score	=	998	Optimized Score	=	1638	Significance	=	10.67	
Residue Identity	=	97%	Matches	=	1648	Mismatches	=	42	
Gaps	=	2	Conservative Substitutions				=	0	

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 1570      1580      1590      1600      1610      1620      1630
  GCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTTGCATATTTCCTACTGCGCTCCAGCCTG
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    | |||
  GCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTTGCATATTTCCTACTGAAATACAG-TGC
     1590      1600      1610      1620      1630      1640      1650

1640      1650      1660      1670      1680      1690 X    1700      1710
  AGTGATAGAGTGAGACTCTGTCTCAAAAAAAAGTATCTCTAAATACAGGATTATAATTTCTGCTTGAGTATG
   ||     || ||     | | |               |  ||     ||| ||  |
  TGTCTATGATTGTTTTTGTTTTGTTGTTTTTTYGAGATCACGYTACTGGGCTC
    1660      1670      1680      1690      1700      X

       1720      1730      1740
  GTGTTAACTACCTTGTATTTAGAAAGATTTC
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